

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 3, 2005, 19:45:51 ; Search time 1246 Seconds
(without alignments)
7120.774 Million cell updates/sec

Title: US-09-982-091A-2
Perfect score: 6604
Sequence: 1 MAALCEEQVFLPEPDISLK.....RFXKDSTPTVKRSIFQLE 1285

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-MAXLEN=200000000 -USER=US0982091@CGN_1_1_560@runat_30092005_162543_10615
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

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22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6604	100.0	4754	9 US-09-982-091A-1	Sequence 1, Appli
2	2695	40.8	4804	20 US-10-357-930-30217	Sequence 30217, A
3	2687	40.7	4756	9 US-09-982-091A-3	Sequence 3, Appli
4	784.5	11.9	5439	24 US-11-097-143-857	Sequence 857, App
5	711.5	10.8	9315	24 US-11-097-143-856	Sequence 856, App
6	498.5	7.5	111206	13 US-10-087-192-1957	Sequence 1957, Ap
7	452	6.8	58837	9 US-09-982-091A-5	Sequence 5, Appli
8	399.5	6.0	20448	24 US-11-097-143-27224	Sequence 27224, A
9	393.5	6.0	547	9 US-09-998-598-480	Sequence 480, App
10	384.5	5.8	484	9 US-09-998-598-268	Sequence 268, App
11	382.5	5.8	9953	24 US-11-097-143-29297	Sequence 29297, A
12	376.5	5.7	10217	21 US-10-956-157-4592	Sequence 4592, Ap
13	373	5.6	7479	19 US-10-697-526-1	Sequence 1, Appli
14	372	5.6	10330	21 US-10-956-157-426	Sequence 426, Appl
15	372	5.6	10330	22 US-10-934-998-25	Sequence 25, Appl
16	371	5.6	10452	11 US-09-968-007A-490	Sequence 490, App
17	371	5.6	10452	21 US-10-843-641A-6960	Sequence 6960, Ap
18	371	5.6	10452	22 US-10-934-998-50	Sequence 50, Appl
19	371	5.6	11167	16 US-10-252-157-188	Sequence 188, App
20	366.5	5.5	3489	11 US-09-894-273-1	Sequence 1, Appli
21	366.5	5.5	3489	15 US-10-294-804-1	Sequence 1, Appli
22	366.5	5.5	3489	20 US-10-194-046-1	Sequence 1, Appli
23	361.5	5.5	24789	24 US-11-097-143-40201	Sequence 40201, A
24	356	5.4	3705	21 US-10-741-849-6132	Sequence 6132, Ap
25	354.5	5.4	4380	17 US-10-094-466-29	Sequence 29, Appl
26	354	5.4	12629	24 US-11-097-143-29296	Sequence 29296, A
27	349.5	5.3	18506	24 US-11-097-143-5629	Sequence 5629, Ap
28	348.5	5.3	4721	24 US-11-097-143-29150	Sequence 29150, A
29	346	5.2	5331	9 US-09-764-176-6	Sequence 6, Appli
30	345.5	5.2	7097	24 US-11-097-143-29149	Sequence 29149, A
31	341	5.2	8910	24 US-11-097-143-27831	Sequence 27831, Ap
32	338.5	5.1	4335	19 US-10-437-963-47851	Sequence 47851, A
33	335.5	5.1	6965	20 US-10-335-053-229	Sequence 229, App
34	334.5	5.1	6900	14 US-10-171-311-163	Sequence 163, App
35	334.5	5.1	6900	22 US-10-764-425-13	Sequence 13, Appl
36	333.5	5.0	7694	16 US-10-096-534-34	Sequence 34, Appl
37	333.5	5.0	7695	11 US-09-968-007A-462	Sequence 462, App
38	333.5	5.0	7695	21 US-10-843-641A-6932	Sequence 6932, Ap
39	333.5	5.0	8063	10 US-09-814-353-21776	Sequence 21776, A
40	333.5	5.0	24971	24 US-11-097-143-27223	Sequence 27223, A
41	331.5	5.0	6861	14 US-10-171-311-161	Sequence 161, App
42	331.5	5.0	6861	17 US-10-341-434-102	Sequence 102, App
43	331.5	5.0	6861	22 US-10-923-035-18	Sequence 18, Appl
44	331.5	5.0	9373	24 US-11-097-143-7772	Sequence 7772, Ap
45	331.5	5.0	12505	24 US-11-097-143-7771	Sequence 7771, Ap

ALIGNMENTS

US-09-982-091A-1

Sequence 1, Application US/09982091A

Patent No. US20020151030A1

GENERAL INFORMATION:

APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY

APPLICANT: KUMAGAI, Akiho

APPLICANT: DUNPHY, William

TITLE OF INVENTION: CLASPIN PROTEINS AND METHODS OF USE THEREOF

FILE REFERENCE: CITI320-1

CURRENT APPLICATION NUMBER: US/09/982,091A

PRIOR FILING DATE: 2002-10-17

PRIOR APPLICATION NUMBER: US 60/241,246

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 3, 2005, 16:09:35 ; Search time 339 Seconds
(without alignments)
6202.406 Million cell updates/sec

Title: US-09-982-091A-2
Perfect score: 6604
Sequence: 1 MAALCEBEEQVFLPEPDISLK.....RRKRDSTPTVKSRISIPQLE 1285

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2695.5	40.8	4756	4	US-09-949-016-4455	Sequence 4455, Ap
2	468	7.1	53737	4	US-09-949-016-16197	Sequence 16197, A
3	366.5	5.5	3489	2	US-08-728-323A-1	Sequence 1, Appl1
4	366.5	5.5	3489	3	US-09-298-568-1	Sequence 1, Appl1
5	366.5	5.5	3489	4	US-09-410-399-1	Sequence 1, Appl1
6	366.5	5.5	3489	4	US-09-894-273-1	Sequence 1, Appl1
7	366.5	5.5	32207	2	US-08-770-379-20	Sequence 20, Appl1
8	366.5	5.5	32207	3	US-08-757-669A-20	Sequence 20, Appl1
9	366.5	5.5	32207	3	US-09-230-371A-20	Sequence 20, Appl1
10	346	5.2	5331	4	US-09-764-176-6	Sequence 6, Appl1
11	345	5.2	6755	3	US-08-931-999-4	Sequence 4, Appl1
12	343.5	5.2	9551	1	US-08-056-200-93	Sequence 93, Appl1

13	343.5	5.2	9551	2	US-08-800-644-93	Sequence 93, Appl1
14	331.5	5.0	6861	4	US-09-949-016-1240	Sequence 1240, Ap
15	331.5	5.0	6861	4	US-09-949-016-1241	Sequence 1241, Ap
16	331.5	5.0	6861	4	US-09-949-016-1242	Sequence 1242, Ap
17	321.5	4.9	8590	4	US-09-949-016-5562	Sequence 5562, Ap
18	321.5	4.9	10300	4	US-09-949-016-636	Sequence 636, App
19	317.5	4.8	38575	4	US-09-949-016-17304	Sequence 17304, A
20	317.5	4.8	119153	4	US-09-949-016-12378	Sequence 12378, A
21	308	4.7	6644	4	US-08-875-435B-5	Sequence 5, Appl1
22	303.5	4.6	5361	3	US-08-973-462-2	Sequence 2, Appl1
23	303.5	4.6	6152	3	US-08-973-462-1	Sequence 1, Appl1
24	300.5	4.6	5200	4	US-08-978-277A-3	Sequence 3, Appl1
25	299.5	4.5	9626	4	US-09-150-867-2	Sequence 2, Appl1
26	296.5	4.5	8503	4	US-09-620-312D-130	Sequence 130, App
27	295.5	4.5	6452	4	US-09-949-016-597	Sequence 597, App
28	295.5	4.5	6453	4	US-09-949-016-1533	Sequence 1533, Ap
29	295.5	4.5	8789	1	US-08-328-254-5	Sequence 5, Appl1
30	293.5	4.4	7453	4	US-09-620-312D-248	Sequence 248, App
31	293.5	4.4	7501	4	US-09-620-312D-249	Sequence 249, App
32	293	4.4	8257	4	US-09-595-684B-30	Sequence 30, Appl1
33	292	4.4	5574	4	US-09-917-254-40	Sequence 40, Appl1
34	292	4.4	5883	4	US-09-949-016-5001	Sequence 5001, Ap
35	292	4.4	6011	4	US-09-949-016-3017	Sequence 3017, Ap
36	290.5	4.4	7596	4	US-09-023-655-1463	Sequence 1463, Ap
37	290	4.4	7571	4	US-09-949-016-4366	Sequence 4366, Ap
38	290	4.4	8146	4	US-09-976-594-725	Sequence 725, App
39	290	4.4	11917	4	US-09-566-921-32	Sequence 32, Appl1
40	290	4.4	101300	4	US-09-949-016-16108	Sequence 16108, A
41	290	4.4	145287	4	US-09-949-016-13530	Sequence 13530, A
42	290	4.4	145287	4	US-09-949-016-13531	Sequence 13531, A
43	286	4.3	6175	4	US-08-875-435B-1	Sequence 1, Appl1
44	284.5	4.3	10136	1	US-08-353-700-2	Sequence 2, Appl1
45	284.5	4.3	10136	5	PCT-US95-16216-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-949-016-4455
Sequence 4455, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4455
LENGTH: 4756
TYPE: DNA
ORGANISM: Human
US-09-949-016-4455

Alignment Scores:
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Score: 2695.50 Matches: 640
Percent Similarity: 60.99% Conservative: 206
Best Local Similarity: 46.14% Mismatches: 309
Query Match: 40.82% Indels: 232
DB: 4 Gaps: 44

US-09-982-091A-2 (1-1285) x US-09-949-016-4455 (1-4756)

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 3, 2005, 14:44:20 ; Search time 6050 Seconds
(without alignments)
8084.725 Million cell updates/sec

Title: US-09-982-091A-2
Perfect score: 6604
Sequence: 1 MAALCEBEOVLEPEDISLK.....RFRDSTPTVKSRIQLE 1285

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09982091@CGN_1_1_3680@runat_30092005.162541.10508 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
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7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1379	20.9	961	6	CA983046	CA983046 AGENCOURT
2	1339	20.3	930	6	CA981092	CA981092 AGENCOURT
3	1288.5	19.5	853	7	CR585850	CR585850 CR585850
4	1189	18.0	922	6	CA985671	CA985671 AGENCOURT
5	1105.5	16.7	933	5	BX756585	BX756585 BX756585
6	1081	16.4	981	6	CA974658	CA974658 AGENCOURT
7	1069	16.2	2075	3	BC018670	BC018670 Homo sapi
8	1056	16.0	864	5	BX783588	BX783588 BX783588
9	1030	15.6	707	1	AL859388	AL859388 AL859388

10	1011	15.3	607	4	BJ041912	BJ041912 BJ041912
11	1003	15.2	915	6	CA791641	CA791641 AGENCOURT
12	1002	15.2	2063	3	AK053847	AK053847 Mus muscu
13	1001	15.2	634	1	AL886670	AL886670 AL886670
14	998.5	15.1	926	5	BU907710	BU907710 AGENCOURT
15	992	15.0	689	1	AL865075	AL865075 AL865075
16	988	15.0	649	1	AL864962	AL864962 AL864962
17	975.5	14.8	640	1	AL878964	AL878964 AL878964
18	975	14.8	647	1	AL878964	AL878964 AL878964
19	960.5	14.5	670	1	AL962969	AL962969 AL962969
20	960	14.5	563	4	BJ029537	BJ029537 BJ029537
21	922	14.0	548	2	AM767107	AM767107 da63a08.y
22	905	13.7	858	1	AL863727	AL863727 AL863727
23	893.5	13.5	955	6	CA982465	CA982465 AGENCOURT
24	874	13.2	527	2	BF427206	BF427206 df63906.y
25	850	12.9	574	1	AL857623	AL857623 AL857623
26	830.5	12.6	751	7	CF749459	CF749459 UI-M-HJO-
27	829.5	12.6	929	5	BQ963412	BQ963412 AGENCOURT
28	804	12.2	864	7	CR416889	CR416889 CR416889
29	790.5	12.0	1027	5	BQ072224	BQ072224 AGENCOURT
30	786	11.9	471	2	BE189872	BE189872 db61g09.y
31	735.5	11.1	663	1	AL891701	AL891701 AL891701
32	728.5	11.0	700	7	CK635361	CK635361 UI-M-HNO-
33	725	11.0	532	5	BX716882	BX716882 BX716882
34	719	10.9	537	4	BI449197	BI449197 dab01b07.
35	712	10.8	420	2	BF612124	BF612124 de91d09.y
36	711	10.8	649	1	AL863524	AL863524 AL863524
37	708.5	10.7	643	1	AL957528	AL957528 AL957528
38	706	10.7	631	1	AL850776	AL850776 AL850776
39	698.5	10.6	630	7	CF724962	CF724962 UI-M-GZO-
40	691.5	10.5	691	7	CF748227	CF748227 UI-M-HJO-
41	668.5	10.1	661	1	AL870060	AL870060 AL870060
42	665	10.1	624	1	AJ392625	AJ392625 AJ392625
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45	646	9.8	582	5	BP313518	BP313518 BP313518

ALIGNMENTS

RESULT 1
LOCUS CA983046 961 bp mRNA linear EST 27-FEB-2003
DEFINITION AGENCOURT_11278764 Wellcome CRC psk egg Xenopus laevis cDNA clone
IMAGE:6870256 5', mRNA sequence.

ACCESSION CA983046
VERSION CA983046.1 GI:27515700

KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)

ORGANISM

Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)
CDNA Library Preparation: N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: XGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM14500 row: f column: 15
High quality sequence start: 11
High quality sequence stop: 710.
Location/Qualifiers

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 3, 2005, 11:21:35 ; Search time 1008 seconds
(without alignments)
7546.496 Million cell updates/sec

Title: US-09-982-091A-2
Perfect score: 6604
Sequence: 1 MAALCEEQVFLPEPDISLK.....RFRKRDSTPTVKSRISIFQLE 1285

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US09982091/runat_30092005_162540_10486/app_query.fasta_1.1479
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09982091@cgn.1.1.523@runat_30092005_162540_10486 -NCPU=6 -ICPU=3
-NO_MMALP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6604	100.0	4754	6	ABK52610 DNA encod
2	2695	40.8	4804	5	ABV30199 Abv30199 Human pro
3	2691	40.7	4414	10	ADC30694 Human nov
4	2687	40.7	4755	6	ABK52611 DNA encod
5	784.5	11.9	5439	4	ABL02411 Drosophila

6	711.5	10.8	9315	4	ABL02410	Ab102410 Drosophila
7	498.5	7.5	111206	11	ACN45152	Acn45152 Mouse gen
8	473.5	7.2	1225	6	ABQ77931	Abq77931 Human mac
9	452	6.8	58837	6	ABK52612	Abk52612 Human cla
10	399.5	6.0	20448	4	ABL19989	Ab119989 Drosophila
11	393.5	6.0	547	6	ABV87169	Abv87169 Human col
12	384.5	5.8	484	6	ABV86957	Abv86957 Human col
13	382.5	5.8	9953	4	ABL21371	Ab121371 Drosophila
14	373	5.6	7479	12	ADQ89533	Adq89533 cDNA enco
15	372	5.6	10330	12	ADK60450	Adk60450 Angiogene
16	372	5.6	10330	12	ADK60751	Adk60751 Angiogene
17	372	5.6	10330	12	ADP73073	Adp73073 Angiogene
18	371	5.6	10452	6	ABL68623	Ab168623 Kidney ca
19	371	5.6	10452	6	ABK84422	Abk84422 Human CDN
20	371	5.6	10452	12	ADK60475	Adk60475 Angiogene
21	371	5.6	10452	12	ADK60776	Adk60776 Angiogene
22	371	5.6	10452	12	ADP73098	Adp73098 Angiogene
23	371	5.6	11167	10	ADE53841	Ad53841 Human pro
24	366.5	5.5	3489	3	AAA30290	Aaa30290 Kaposi's
25	366.5	5.5	3489	4	AAF82901	Aaf82901 Nucleotid
26	366.5	5.5	3489	6	ABA93487	Ab93487 Kaposi's
27	366.5	5.5	3489	12	ADU65095	Ad65095 HHV8 DNA
28	366.5	5.5	32207	2	AAV73805	Aav73805 KSHV LUR
29	366.5	5.5	137507	2	AAV19941	Aav19941 KSHV long
30	366.5	5.5	137508	12	ADN12162	Adn12162 Human her
31	361.5	5.5	24789	4	ABL28640	Ab128640 Drosophila
32	356	5.4	3705	12	ADP98647	Adp98647 C. albica
33	354.5	5.4	4380	6	ABS78735	Ab78735 DNA encod
34	354.5	5.4	4510	8	ACC46305	Acc46305 Human dit
35	354	5.4	12629	4	ABL21370	Ab121370 Drosophila
36	350.5	5.3	5281	4	AAF87096	Aaf87096 AAP-2 cod
37	349.5	5.3	18506	4	ABL05592	Ab105592 Drosophila
38	348.5	5.3	4721	4	ABL21273	Ab121273 Drosophila
39	345.5	5.2	7097	4	ABL21272	Ab121272 Staphyloc
40	345	5.2	6755	2	AAV21511	Aav21511 Tumour-as
41	343.5	5.2	9551	2	AAZ22301	Aaz22301 cDNA enco
42	342	5.2	4755	13	ACN37449	Acn37449 Tumour-as
43	341	5.2	8910	4	ABL03395	Ab103395 Drosophila
44	335.5	5.1	6965	10	ADD29780	Add29780 Human cer
45	334.5	5.1	6900	8	ACF12910	Acf12910 Human cer

ALIGNMENTS

RESULT 1	
ABK52610	standard; DNA; 4754 BP.
ID	ABK52610
XX	
AC	ABK52610;
XX	
DT	27-AUG-2002 (first entry)
XX	
DE	DNA encoding Xenopus Claspin protein.
XX	
KW	Chk1 protein; SQ/TQ motif; isoelectric point; cell cycle progression;
KW	nuclear localisation signal; DNA replication checkpoint; benign neoplasm;
KW	cell proliferative disorder; malignant neoplasm; frog; claspin; gene; ds.
XX	
OS	Xenopus sp.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	71..3928
FT	/*tag= a
FT	/product= "Xenopus Claspin protein"
XX	
PN	WO200233115-A2.
XX	
PD	25-APR-2002.
XX	
PF	17-OCT-2001; 2001WO-US032316.
XX	
PR	17-OCT-2000; 2000US-0241246P.
XX	

